

Using advanced imaging and analysis to find a gene that influences maize Root System Architecture (RSA) and nitrogen relations

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Understanding plant architecture can lead to identifying breeding targets impacting crop yield, physiology, and efficiency. The genetics controlling root system architecture (RSA), in particular, are not well-understood due to the difficulty in accurately capturing and measuring complex morphological traits. Here we use 2D and 3D imaging to identify and verify a candidate gene underlying a maize Quantitative Trait Locus (QTL) for altered root system architecture. The gene was mapped in a population derived from the Illinois Long Term Protein Selection Strains (ILTPS), which have diverged for nitrogen uptake capacity. We extracted root traits via Digital Imaging of Root Traits (DIRT) from hundreds of 2D images of root crowns of mature field-grown ILTPS maize. We performed a Genome-Wide Association Study (GWAS) to identify a QTL controlling multiple root crown traits. Only one gene was within the local region of Linkage Disequilibrium (LD) of this QTL, and subsequent nanopore sequencing and quantitative PCR revealed lesions in the promoter which reduced gene expression, presumably driving the divergent phenotypes. An analysis of 3D models generated from X-ray Computed Tomography of root crowns verified that ILTPS lines containing the high-versus-low expressing alleles had significantly different RSAs, for example, in their Solidity, which suggests they explore the soil differently. An ongoing field experiment aims to understand how these different RSAs affect plant nitrogen uptake. Additionally, we generated CRISPR-Cas9 mutants in maize to investigate this gene's role in RSA and nitrogen relations in maize.